

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
Carroll, Joseph M.

<120> 23565, A NOVEL HUMAN ZINC
CARBOXYPEPTIDASE FAMILY MEMBER AND USES THEREOF

<130> 10448-142001

<150> 60/269,440

<151> 2001-02-16

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (160)...(1467)

<221> misc_feature

<222> 10, 1685

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cccaaggaaa	gccctgaag	ctcaccagga	ggaagaagc	atg cag ggc act cct		174
				Met Gln Gly Thr Pro		
				1	5	

gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg acg ctc	222
Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg Thr Leu	
10 15 20	

ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg aat ttc	270
Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met Asn Phe	
25 30 35	

aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag cag ctt	318
Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys Gln Leu	
40 45 50	

tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg gac ttc	366
Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val Asp Phe	
55 60 65	

tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga gtt cct	414
Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg Val Pro	

FASTSEQ FOR WINDOWS

70	75	80	85	
ttc tcc gaa ctg aaa gac atc aaa gct tat ctg gag tct cat gga ctt	462			
Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu Glu Ser His Gly Leu				
90	95	100		
gct tac agc atc atg ata aag gac atc cag gtg ctg ctg gat gag gaa	510			
Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val Leu Leu Asp Glu Glu				
105	110	115		
aga cag gcc atg gcg aaa tcc cgc cgg ctg gag cgc agc acc aac agc	558			
Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu Arg Ser Thr Asn Ser				
120	125	130		
ttc agt tac tca tca tac cac acc ctg gag gag ata tat agc tgg att	606			
Phe Ser Tyr Ser Ser Tyr His Thr Leu Glu Glu Ile Tyr Ser Trp Ile				
135	140	145		
gac aac ttt gta atg gag cat tcc gat att gtc tca aaa att cag att	654			
Asp Asn Phe Val Met Glu His Ser Asp Ile Val Ser Lys Ile Gln Ile				
150	155	160	165	
ggc aac agc ttt gaa aac cag tcc att ctt gtc ctg aag ttc agc act	702			
Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val Leu Lys Phe Ser Thr				
170	175	180		
gga ggt tct cgg cac cca gcc atc tgg atc gac act gga att cac tcc	750			
Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp Thr Gly Ile His Ser				
185	190	195		
cgg gag tgg atc acc cat gcc acc ggc atc tgg act gcc aat aag att	798			
Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp Thr Ala Asn Lys Ile				
200	205	210		
gtc agt gat tat ggc aaa gac cgt gtc ctg aca gac ata ctg aat gcc	846			
Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr Asp Ile Leu Asn Ala				
215	220	225		
atg gac atc ttc ata gag ctc gtc aca aac cct gat ggg ttt gct ttt	894			
Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro Asp Gly Phe Ala Phe				
230	235	240	245	
acc cac agc atg aac cgc tta tgg cgg aag aac aag tcc atc aga cct	942			
Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn Lys Ser Ile Arg Pro				
250	255	260		
gga atc ttc tgc atc ggc gtg gat ctc aac agg aac tgg aag tgc ggt	990			
Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg Asn Trp Lys Ser Gly				
265	270	275		
ttt gga gga aat ggt tct aac agc aac ccc tgc tca gaa act tat cac	1038			
Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys Ser Glu Thr Tyr His				
280	285	290		
ggg ccc tcc cct cag tcg gag tcg gag gtg gct gcc ata gtg aac ttc	1086			
Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala Ile Val Asn Phe				
295	300	305		

atc aca gcc cat ggc aac ttc aag gct ctg atc tcc atc cac agc tac 1134
 Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile Ser Ile His Ser Tyr
 310 315 320 325

tct cag atg ctt atg tac cct tac ggc cga ttg ctg gag ccc gtt tca 1182
 Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu Leu Glu Pro Val Ser
 330 335 340

aat cag agg gag ttg tac gat ctt gcc aag gat gcg gtg gag gcc ttg 1230
 Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp Ala Val Glu Ala Leu
 345 350 355

tat aag gtc cat ggg atc gag tac att ttt ggc agc atc agc acc acc 1278
 Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly Ser Ile Ser Thr Thr
 360 365 370

ctc tat gtg gcc agt ggg atc acc gtc gac tgg gcc tat gac agt ggc 1326
 Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp Ala Tyr Asp Ser Gly
 375 380 385

atc aag tac gcc ttc agc ttt gag ctc cgg gac act ggg cag tat ggc 1374
 Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp Thr Gly Gln Tyr Gly
 390 395 400 405

ttc ctg ctg ccg gcc aca cag atc atc ccc acg gcc cag gag acg tgg 1422
 Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr Ala Gln Glu Thr Trp
 410 415 420

atg gcg ctt cgg acc atc atg gag cac acc ctg aat cac ccc tac 1467
 Met Ala Leu Arg Thr Ile Met Glu His Thr Leu Asn His Pro Tyr
 425 430 435

tagcagcacg actgagggca ggaggctcca tccttctccc caaggtctgt ggctcctccc 1527
 gaaacccaag ttatgcatcc ccattcccat gccctcatcc cgacctctta gaaaataaat 1587
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<210> 2

<211> 436

<212> PRT

<213> Homo sapiens

<400> 2

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 20 25 30
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 35 40 45
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 50 55 60
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 65 70 75 80
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu
 85 90 95
 Glu Ser His Gly Leu Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val

205720"5653200T

100 105 110
 Leu Leu Asp Glu Glu Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu
 115 120 125
 Arg Ser Thr Asn Ser Phe Ser Tyr Ser Ser Tyr His Thr Leu Glu Glu
 130 135 140
 Ile Tyr Ser Trp Ile Asp Asn Phe Val Met Glu His Ser Asp Ile Val
 145 150 155 160
 Ser Lys Ile Gln Ile Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val
 165 170 175
 Leu Lys Phe Ser Thr Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp
 180 185 190
 Thr Gly Ile His Ser Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp
 195 200 205
 Thr Ala Asn Lys Ile Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr
 210 215 220
 Asp Ile Leu Asn Ala Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro
 225 230 235 240
 Asp Gly Phe Ala Phe Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn
 245 250 255
 Lys Ser Ile Arg Pro Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg
 260 265 270
 Asn Trp Lys Ser Gly Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys
 275 280 285
 Ser Glu Thr Tyr His Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala
 290 295 300
 Ala Ile Val Asn Phe Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile
 305 310 315 320
 Ser Ile His Ser Tyr Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu
 325 330 335
 Leu Glu Pro Val Ser Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp
 340 345 350
 Ala Val Glu Ala Leu Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly
 355 360 365
 Ser Ile Ser Thr Thr Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp
 370 375 380
 Ala Tyr Asp Ser Gly Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp
 385 390 395 400
 Thr Gly Gln Tyr Gly Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr
 405 410 415
 Ala Gln Glu Thr Trp Met Ala Leu Arg Thr Ile Met Glu His Thr Leu
 420 425 430
 Asn His Pro Tyr
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<210> 3

<211> 1311

<212> DNA

<213> Homo sapiens

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caggttcttc	gagtcctggc	caaagatgag	aagcagcttt	cacttctcgg	ggatctggag	180
ggcctgaaac	cccagaaggt	ggacttctgg	cgtggcccag	ccaggcccag	cctccctgtg	240
gatatgagag	ttcctttctc	cgaactgaaa	gacatcaaag	cttatctgga	gtctcatgga	300
cttgcttaca	gcatcatgat	aaaggacatc	caggtgctgc	tgatgagga	aagacaggcc	360
atggcgaaat	cccgccggct	ggagcgcagc	accaacagct	tcagttactc	atcataccac	420

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accctggagg agatatatag ctggattgac aactttgtaa tggagcattc cgatattgtc 480
tcaaaaattc agattggcaa cagctttgaa aaccagtcca ttcttgcct gaagttcagc 540
actggagggtt ctcggcaccc agccatctgg atcgacactg gaattcactc ccgggagtg 600
atcacccatg ccaccggcat ctggactgcc aataagattg tcagtgatta tggcaaagac 660
cgtgtcctga cagacatact gaatgccatg gacatcttca tagagctcgt cacaaaccct 720
gatgggtttg cttttaccca cagcatgaac cgcttatggc ggaagaacaa gtccatcaga 780
cctggaatct tctgcatcgg cgtggatctc aacaggaact ggaagtcggg ttttggagga 840
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tcggaggtgg ctgccatagt gaacttcatac acagcccata gcaacttcaa ggctctgatc 960
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accgtcgact gggcctatga cagtggcatc aagtacgcct tcagctttga gctccgggac 1200
actgggcagt atggcttctt gctgccggcc acacagatca tccccacggc ccaggagacg 1260
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<210> 4

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 4

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Gly Arg Asp Leu Lys Val Leu Lys Ile Ser Asp Asn Pro Ala Thr Gly
35     40     45
Glu Asn Glu Pro Glu Val Phe Ala Val Ala Gly Trp Ile His Ala Arg
50     55     60
Glu Trp Val Thr Ser Ala Thr Leu Leu Trp Leu Leu Lys Glu Leu Val
65     70     75     80
Ala Asn Tyr Gly Ser Asp Lys Thr Ile Thr Lys Leu Leu Asp Gly Leu
85     90     95
Asp Leu Phe Tyr Ile Leu Pro Val Phe Asn Pro Asp Gly Tyr Ala Tyr
100    105    110
Ser Ile Thr Thr Asp Ser Tyr Arg Met Trp Arg Lys Thr Arg Ser Pro
115    120    125
Asn Ala Gly Ser Phe Cys Val Gly Thr Asp Pro Asn Arg Asn Trp Tyr
130    135    140
Ala Gln Trp Gly Gly Met Gly Ala Ser Ser Tyr Ser Pro Cys Ser Glu
145    150    155    160
Thr Tyr Glu Gly Thr Ala Pro Phe Ser Glu Pro Glu Thr Lys Ala Val
165    170    175
Glu Asp Phe Ile Arg Ser Trp Leu Gly Gly Gly Lys Gln Asn Ile Lys
180    185    190
Ala Tyr Ile Thr Phe His Ser Tyr Ser Gln Leu Leu Leu Tyr Pro Tyr
195    200    205
Gly Tyr Asp Tyr Asn Leu Asn Pro Asp Ala Asn Asp Leu Asp Glu Leu
210    215    220
Ser Asp Leu Lys Ile Ala Ala Asp Ala Leu Ser Ala Arg His Gly Thr
225    230    235    240
Tyr Tyr Thr Leu Gly Leu Pro Gly Ser Ser Thr Ile Tyr Pro Ala Ser
245    250    255

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CCDS: E03037

Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp Val Gly Ile Ile Lys Tyr
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 Ala Phe Thr Phe Glu Leu Arg Pro Asp Thr Gly Ser Tyr Gly Asn Pro
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<210> 5
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

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 Tyr Glu Gly Arg Pro Ile Lys Val Leu Lys Ile Lys Pro Ala Val Phe
 35 40 45
 Ile Asp Ala Gly Ile His Ala Arg Glu Trp Ile Ala Pro Ala Thr Ala
 50 55 60
 Leu Tyr Leu Ile Asn Gln Leu Leu Thr Asn Glu Thr Glu Tyr Ser Lys
 65 70 75 80
 Asp Pro Asp Asp Glu Gly Ser Val Thr Lys Leu Leu Asp Lys Leu Asp
 85 90 95
 Trp Tyr Ile Val Pro Val Met Asn Pro Asp Gly Tyr Glu Tyr Thr His
 100 105 110
 Thr Ser Thr Asp Arg Leu Trp Arg Lys Asn Arg Ser Pro Asn Gly Ala
 115 120 125
 Ser Gly Ser Gln Gly Thr Trp Tyr Asn Cys Tyr Gly Val Asp Leu Asn
 130 135 140
 Arg Asn Phe Asp Phe His Asn Trp Gly Glu Ile Gly Gly Ser Ser Ser
 145 150 155 160
 Leu Pro Cys Ser Glu Thr Tyr Ala Gly Ser Ser Pro Phe Ser Glu Trp
 165 170 175
 Glu Pro Glu Thr Lys Ala Leu Leu Asp Phe Ile Leu Ser Asn Glu Ile
 180 185 190
 Gly Lys Gly Arg Ile Lys Ala Tyr Ile Ser Leu His Ser Tyr Ser Gln
 195 200 205
 Leu Leu Leu Tyr Pro Tyr Gly Tyr Thr Asn Ala Thr Val Pro Pro Asn
 210 215 220
 Gly Glu Asp Leu His Lys Glu Val Ala Lys Ala Ala Lys Ala Ile
 225 230 235 240
 Gly Asp Tyr Tyr Phe Gly Gly Thr Leu Tyr Thr Pro Gly Ser Ser Ser
 245 250 255
 Ala Asp Pro Asp Leu Asp Ile Thr Leu Tyr Pro Ala Ser Gly Gly Ser
 260 265 270
 Asp Asp Trp Ala Tyr Gly Thr Leu Lys Gly Val Lys Tyr Ser Tyr Thr
 275 280 285
 Ile Glu Leu Arg Asp Thr Gly Asp Asp Ala Gly Arg Tyr Gly Phe Leu
 290 295 300
 Leu Pro Pro Ser Cys Val Lys Pro Val Arg Met Glu Gln Ile Ile Pro
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 Thr Gly Glu Glu

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<210> 6
 <211> 82
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<400> 6
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 Lys Asp Leu Glu Asn Thr Glu His Leu Glu Leu Asp Phe Trp Lys Pro
 20 25 30
 Asp Ser Ala Thr Pro Ile Lys Pro Gly Ser Thr Val Asp Phe Arg Val
 35 40 45
 Pro Ala Glu Asp Ile Gln Ala Val Lys Ser Phe Leu Glu Gln Ser Gly
 50 55 60
 Ile His Tyr Glu Val Leu Ile Glu Asp Val Gln Glu Leu Leu Glu Glu
 65 70 75 80
 Gln Phe

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